

004350 4592450

```

GAATTCGGCTCGAATCATTGCTCTGTTCCGGTATCGATTGAGAAACCGAACTTGTGATCGA
1 ----- 60
TAACAAGTCATTCAACACGGCGAAGATGTCTATGCGGTATAACAGAATATTGGAGAAAT
61 ----- 120
GCTCGCAAACTCGAAATTGTCCCGATAAAATGATTAACTTGAAGGGGCTAATGTAAGT
121 ----- 180
TATCTGATGTTTCTACAATTAAAAAAATTGTTTTTTTCCAAATTAATTTTCGAAGATT
181 ----- 240
AACGAAAAACGATTAAAAATCAATAAAACGCAATAAAGAGGGCTTGGCTTTCTTTTAAT
241 ----- 300
TTAAATTATAATTTTCTGATTGTTGTATGAAGCTACAAAATGTAAGTGTATTTGATTTC
301 ----- 360
AATATTGTATTACAGGGTTCGGATTCTCGGCAATATCAGCGACAGTGAAGATTAGAA
361 ----- 420
GAAGGACGTGTGACAATCACTAAGTCAAAGAGGGAAAGGATAAAGGATTGTGATTTTCA
421 ----- 480
CTGTTTTACTCATTCCGCTTTTAAATAAGAACTATATGCCGATTTCGGGATATATTTTC
481 ----- 540
TTTATTAGGCTCTCACATTCCCTGTACAATGTTTCTACCAATAAACTGCAITTTTATCT
541 ----- 600
GAAAATTCGAATTTATTTTGTCTACTTTTACTCGTTGCATTGAGATCAGCATATCTT
601 ----- 660
CCGGTCTATTATATCAACGATTTTATAAATTAGTACTCCTTCATGTTTAAATTCATT
661 ----- 720
TTATCTGTAAGCTTTACTGTATTTTTTAAATCTTTCTTGCTTCTATCTGATTATACAA
721 ----- 780
TGTCTTTTACTCATTTTCAAGGTATTTTATGCCCTCACAAATTTATGCACATTTCCGGCTT
781 ----- 840
GGAGATTTATCCTCTATATTACATGCCGTGTTTTTTAAAGGATATAATGTTTAACAAATA
841 ----- 900
ATTTTTTATCAATGCTATTGTATATTCTCCAGCTAACCGTTGTTTCGAAAACATCACCTA
901 ----- 960
GCATTTTTAAATTCACAAAATCTTGCTTCCTTATAATCAAGAAGATTTTTCAGATGCTCT
961 ----- 1020
M L C
GGGAAATCGAATGCCCGCGCTTTGAGCACGGCACACACGAGGCTCATCCACGACTTTGAAC
1021 ----- 1080
E I E C R A L S T A H T R L I H D F E P
10      20
T n1162
CACGTGACGCATTGACTTATTTAGAAGGCAAAAACATTTTCACAGAAGATCATTCTGAAC
1081 ----- 1140
R D A L T Y L E G K N I F T E D H S E L
30      40
TTATCAGTAAAAATGTCAACTCGCCTCGAGAGGATCGCCAATTTTCTTGAATCTATCGAC
1141 ----- 1200
I S K M S T R L E R I A N F L R I Y R R
50      60
GTCAAGCTTCTGAACTTGGACCACTCATCGACTTTTCAACTACAACAATCAAAAGTCACC
1201 ----- 1260
Q A S E L G P L I D F F N Y N N Q S H L
70      80
TTGCTGATTTCTCGAAGACTACATCGATTTTGGGATAAATGAGCCAGATCTACTTCGTC
1261 ----- 1320
A D F L E D Y I D F A I N E P D L L R P
90      100
CAGTAGTGATTGCTCCACAATTTTCCCGACAAATGCTCGATAGGAACTATTGCTTGGGA
1321 ----- 1380
V V I A P Q F S R Q M L D R K L L L G N
110      120

```

FIGURE 1

Fig 10

T n2274

1381 ATGTTCCAAAACAAATGACATGCTATATTCGAGAGTATCACGTGGATCGAGTGATCAAAA 1440
 V P K Q M T C Y I R E Y H V D R V I K K
 130 140

Intron 1

1441 AGCTCGACGAGATGTGTGATTTAGCTGAGAAAACCTGGAAGCTCTCGTGTATTATTAATC
 L D E M C D L D
 150

1501 TTGCTTAAACTTCAGACTCCTTTTTCTGTTTCTACACGGCCGAGCTGGATCCGGAAAAT 1560
 S F F L F L H G R A G S G K S
 160

Intron 2

1561 CAGTAATTGCATCACAAGCTCTTTTGGAAATCTGACCAACTTATTGGAAATGAGTGGTAT 1620
 V I A S Q A L S K S D Q L I G I
 170 180

1621 TATCTGAATCTACGGATCTTCATTCTATTACACAAATTATGATTCAATCGTTTGGCTCAA 1680
 N Y D S I V W L K
 190

1681 AGATAGTGAACAGCTCCAAAATCTACATTGATTTATTACGGATATTTTGTGATGCT 1740
 D S G T A P K S T F D L F T D I L L M L
 200 210

A n1920/n2247

Intron 3

1741 AAAGTGAGTGAATAGAGTGCATGTAACATTACCATGATTTTGGAAATTATGAAAATTTGA 1800
 K
 CCTGGTTAGCTTTTAATTGATATTTCTGACGCTTGCATGTTTGTGTGTTTGAAGACG
 1801 1860
 AGCCCGTGTGTGTAGCGACACGGATGACTCGCATTCGATCACCGACTTCATTAAACCGTGT
 1861 1920

A n2273

1921 TCTTTCAACAAGCGAAGACGATCTTCTCAATTTCCCATCGGTGGAGCATGTCACGTCAGT 1980
 S E D D L L N F P S V E H V T S V
 220

Intron 4

1981 TGTACTCAAAGGATGTAAGTTGCTTGCCGATTCTGGTACAATATCTTAAATTATTGGT 2040
 V L K R M
 230

2041 TTTTAGATCTGCAACGCACCTCATTGATCGTCCAAATACCTTATTGGTATTGATGACGTA 2100
 I C N A L I D R P N T L F V F D D V
 240 250

A n1948 T n1947

2101 GTTCAAGAAGAAACAATTTCGTTGGGGCTCAGGAGCTACGTCTTCGATGTCTTGTAAGTACT 2160
 V Q E E T I R W A Q E L R L R C L V T T
 260 270

2161 CGTGACGTGGAAATATCAAATGCTGCTTCTCAAACATGCGAATTCATTGAAGTGACATCA 2220
 R D V E I S N A A S Q T C E F I E V T S
 280 290

FIGURE 1

[illegible]

FIGURE 1

[illegible]

FIGURE 1

004300 240345Z

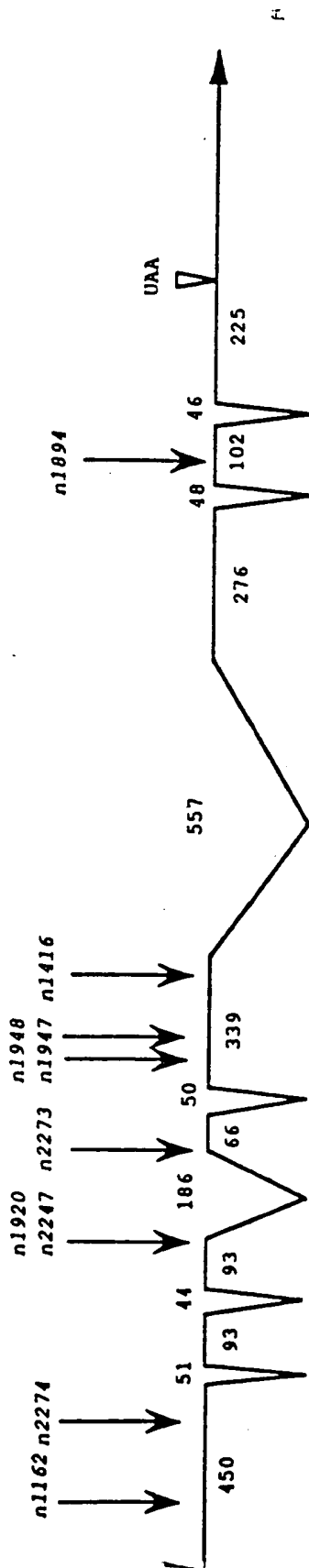


FIGURE 2

	10	12	14	18	21
	X	Y	Z	-X	-Z
Calcium-binding loop consensus	D	N	S	T	E
		D	N	S	
			D	E	
				Q	
				D	
				N	
EF-hand consensus	<u>O * O * O G * * O * * E</u>				
ced-4 sequence 1	Y	N	N	Q	S
sequence 2	S	L	E	I	D
Parvalbumin (carp)	D	Q	D	K	S
(hake)	D	Q	D	K	D
(ray)	D	S	D	G	D
SCBP (<i>Amphioxus</i> I)	D	I	N	K	D
ICaBP (bovine)	A	K	E	G	D
	D	K	N	G	D
Troponin C (rabbit)	D	A	D	G	G
	D	E	D	G	S
	D	R	N	A	D
	D	K	N	N	D
Calmodulin (bovine)	D	K	D	G	N
Trypsinogen	L	G	E	D	N
Fibrinogen	D	N	D	N	D
Villin	G	V	D	P	S
GBP	D	L	N	K	D

FIGURE 3

ced-3 Genomic Sequence

```

1  AGATCTGAAATAAGGTGATAAATTAATAAATTAAGTGTATTTCTGAGGAAATTTGACTGT
   +-----+-----+-----+-----+-----+-----+
61  TTTAGCACAAATTAATCTTGTTTCAGAAAAAAGTCCAGTTTCTAGATTTTCCGTCTTA
   +-----+-----+-----+-----+-----+-----+
121  TTGTCGAATTAATATCCCTATTATCACTTTTTCATGCTCATCCTCGAGCGGCACGTCCTC
   +-----+-----+-----+-----+-----+-----+
181  AAAGAATTGTGAGAGCAAACGCGCTCCCATTTGACCTCCACACTCAGCCGCCAAAACAAAC
   +-----+-----+-----+-----+-----+-----+
241  GTTCGAACATTCGTGTGTTGTGCTCCTTTTCCGTTATCTTGCACTCATCTTTTGTGCTTT
   +-----+-----+-----+-----+-----+-----+
301  TTTTCTTTGTTCTTTTGTGTAACGTGTTGCTAAGCAATTATTACATCAATTGAAGAAAA
   +-----+-----+-----+-----+-----+-----+
361  GGCTCGCCGATTTATTGTTGCCAGAAAGATTCTGAGATTCTCGAAGTCGATTTTATAATA
   +-----+-----+-----+-----+-----+-----+
421  TTTAACCTTGGTTTTTGCATTGTTTCGTTTAAAAAACCACTGTTTATGTGAAAAACGAT
   +-----+-----+-----+-----+-----+-----+
481  TAGTTTACTAATAAACTACTTTTAAACCTTTACCTTACCTCACCCTCCGTGTTTCATG
   +-----+-----+-----+-----+-----+-----+
541  GCTCATAGATTTTCGATACTCAAAATCCAAAAATAAATTTACGAGGGCAATTAATGTGAAA
   +-----+-----+-----+-----+-----+-----+
601  CAAAAACAATCCTAAGATTTCCACATGTTTGACCTCTCCGGCACCTTCTTCCTTAGCCCC
   +-----+-----+-----+-----+-----+-----+
661  ACCACTCCATCACCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTGTGTAT
   +-----+-----+-----+-----+-----+-----+
721  CTCATTTGGTATGCTCTTTTCGATTTTATAGCTCTTGTGCGCAATTTCAATGCTTTAAAC
   +-----+-----+-----+-----+-----+-----+
781  AATCCAAATCGCATTATATTTGTGCATGGAGGCAAATGACGGGGTTGGAATCTTAGATGA
   +-----+-----+-----+-----+-----+-----+
841  GATCAGGAGCTTTCAGGGTAAACGCCCGGTTTCAATTTGTACCACATTTTCATATTTTCCT
   +-----+-----+-----+-----+-----+-----+
901  GTCGTCCTTGGTATCCTCAACTTGTCCCGGTTTTGTTTTCGGTACACTCTTCCGTGATGC
   +-----+-----+-----+-----+-----+-----+
961  CACCTGTCTCCGTCTCAATTATCGTTTAGAAATGTGAAGTGTCCAGATGGGTGACTCATA
   +-----+-----+-----+-----+-----+-----+
1021  TTGCTGCTGCTACAATCCACTTTCTTTCTCATCGGCAGTCTTACGAGCCCATCATAAAC
   +-----+-----+-----+-----+-----+-----+
1081  TTTTTTTTCCGCGAAATTTGCAATAAACCGGCCAAAAACTTTCTCCAAATTGTTACGCAA
   +-----+-----+-----+-----+-----+-----+
1141  TATATACAATCCATAAGAATATCTTCTCAATGTTTATGATTTCTTCGAGCACTTTCTCT
   +-----+-----+-----+-----+-----+-----+
1201  TCGTGTGCTAACATCTTATTTTATAATATTTCCGCTAAAATTCCGATTTTGTAGTATTA
   +-----+-----+-----+-----+-----+-----+
1261  ATTTATCGTAAATATCATAATAGCACCAGAACTACTAAAAATGGTAAAGCTCCTTT
   +-----+-----+-----+-----+-----+-----+
                                     Repeat 1
1321  TAAATCGGCTCGACATTATCGTATTAAGGAATCACAAAATTCTGAGAATGCGTACTGCGC
   +-----+-----+-----+-----+-----+-----+
                                     Repeat 1
1381  AACATATTTGACGGCAAAATATCTCGTAGCGAAACTACAGTAATTCTTTAAATGACTAC
   +-----+-----+-----+-----+-----+-----+
                                     Repeat 1
1441  TGTAGCGCTTGTGTCGATTTACGGGCTCAATTTTGAATAATTTTTTTTTTTCGAATTT
   +-----+-----+-----+-----+-----+-----+

```

FIGURE 4

[illegible]

FIGURE 4

Repeat 2

3481 TTTTTCATTCAAGATATGCTTATTAACACATATAATTATCATTAAATGTGAATTTCTTG 3540
 3541 TAGAAATTTGGGCTTTTCGTTCTAGTATGCTCTACTTTTGAAATTGCTCAACGAAAAA 3600
 3601 TCATGTGGTTTGTTTCATATGAATGACGAAAAATAGCAATTTTATATATTTTCCCCTAT 3660
 3661 TCATGTTGTGCAGAAAAATAGTAAAAAGCGCATGCATTTTCGACATTTTACATCGA 3720
 3721 ACGACAGCTCACTTCACATGCTGAAGACGAGAGACGCGGAGAAATACCACACATCTTCT 3780
 Repeat 2
 3781 GCGTCTCTCGTCTTCAGCATGTGAATGGGATCTCGGTCGATGTAAAAAATGTGGAATA 3840
 3841 ATGTAAAAAATGCATGCGTTTTTTTACACTTTTCTGCACAAATGAATAGGGGGAAATGT 3900
 3901 ATTAAAAATACATTTTTTGTATTTTTCAACATCACATGATTAACCCCATTTATTTTTTCGTT 3960
 3961 GAGCAACTTAAAAAGTAGAGAATATTAGAGCGAAAACCAAAATTTCTCAAGATATTACC 4020
 4021 TTTATTGATAATTATAGATGTTAATAAGCATATCTTGAATGAAAGTCAGCAAAAATATGT 4080
 4081 GCGAAACACCTGAAAAAATCAAAAATTCTGCGAAAATTGAAAAATGCATTAAATACA 4140
 4141 TTTTGCATTTTCTACATCACATGAATGTAGAAAATTTAAAGGGAAATCAAAATTTCTA 4200
 4201 GAGGATATAATTGAATGAAACATTGCGAAATTTAAATGTGCGAAACGTCAAAAAGAGGA 4260
 4261 AATTTGGGTATCAAAATCGATCCTAAAACCAACACATTTTCAGCATCCGCCAACTCTTCAT 4320
 S A N S S F
 180

FIGURE 4

4321 TCACCGGATGCTCTTCTCTCGGATACAGTTCAAGTCGTAATCGCTCATTGAGCAAAGCTT 4380
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 T G C S S L G Y S S S R N R S F S K A S
 190 200
 4381 CTGGACCAACTCAATACATATTCCATGAAGAGGATATGAACCTTGTGCGATGCACCAACCA 4440
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 G P T Q Y I F H E E D M N F V D A P T I
 210 220
 4441 TAAGCCGTGTTTTTCGACGAGAGAAAACCATGTACAGAACTTCTCGAGTCCTCGTGAATGT 4500
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 S R V F D E K T M Y R N F S S P R G M C
 230 240
 4501 GCCTCATCATAAATAATGAACACTTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG 4560
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 L I I N N E H F E Q M P T R N G T K A D
 250 260
 4561 ACAAGGACAATCTTACCAATTTGTTTCAGATGCATGGGCTATACGGTTATTTGCAAGGACA 4620
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 K D N L T N L F R C M G Y T V I C K D N
 270 280
 | intron 4
 4621 ATCTGACGGGAAGGTACGGCGAAATTATATTACCCAAACGCGAAATTGCCATTTTGCG 4680
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 L T G R
 Repeat 3
 ----->
 4681 CCGAAAATGTGGCGCCCGGTCTCGACACGACAATTTGTGTTAAATGCAAAAATGTATAAT 4740
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4741 TTTGCAAAAACAAAATTTTGAACCTCCGCGAAAATGATTTACCTAGTTTCGAAATTTTC 4800
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4801 GTTTTTTCCGGCTACATTATGTGTTTTTCTTAGTTTTCTATAATATTTGATGTAAAAA 4860
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4861 ACCGTTTGTAATTTTCAGACAATTTCCGCATACAAAACCTTGATAGCACGAAATCAATT 4920
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4921 TTCTGAATTTTCAAAAATTATCCAAAATGCACAATTTAAAATTTGTGAAAATTGGCAAAC 4980
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4981 GGTGTTTCAATATGAAATGTATTTTAAAAACCTTAAAAACCACTCCGAAAAGCAATAA 5040
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5041 AAATCAAAACACGTCACAATTCAAATTCAAAAGTTATTCATCCGATTGTTTTATTTTG 5100
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5101 CAAAATTTGAAAAAATCATGAAGGATTTAGAAAAGTTTATAACATTTTTTCTAGATTTT 5160
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5161 TCAAAATTTTTTTTAACAATCGAGAAAAAGAGAATGAAAATCGATTTTAAAAATATCC 5220
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 Repeat 3
 <-----
 5221 ACAGCTTCGAGAGTTTGAAATTACAGTACTCCTTAAAGGCGCACACCCCATTTGCATTGG 5280
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

 5281 ACCAAAAATTTGTCGTGTCGAGACCAGGTACCGTAGTTTTTGTGCAAAAATTCACCAT 5340
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5341 TGGACAATAAACCTTCCTAATCACCAAAAAGTAAAATTGAAATCTTCGAAAAGCCAAAAA 5400
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

FIGURE 4

5401 ATTCAAAAAAAAAAGTCGAATTCGATTTTTTTTTTGGTTTTTTGGTCCCAAAAACCAAAA 5460
 -----+-----+-----+-----+-----+-----+-----+-----+
 5461 AAATCAATTTTCTGCAAAATACCAAAAAGAAACCCGAAAAAATTTCCAGCCTTGTTCCT 5520
 -----+-----+-----+-----+-----+-----+-----+-----+
 5521 AATGTAAACTGATATTTAATTTCCAGGGAATGCTCCTGACAATTCGAGACTTTGCCAAAC 5580
 -----+-----+-----+-----+-----+-----+-----+-----+
 G M L L T I R D F A K H
 290 300
 5581 ACGAATCACACGGAGATTCTGCGATACTCGTGATTCTATCACACGGAGAAGAGAATGTGA 5640
 -----+-----+-----+-----+-----+-----+-----+-----+
 E S H G D S A I L V I L S H G E E N V I
 310 320
 5641 TTATTGGAGTTGATGATATACCGATTAGTACACAGAGATATATGATCTTCTCAACGCGG 5700
 -----+-----+-----+-----+-----+-----+-----+-----+
 I G V D D I P I S T H E I Y D L L N A A
 330 340
 A(n2433)
 5701 CAAATGCTCCCCGTCTGGCGAATAAGCCGAAATCGTTTTTGTGCAGGCTTGTGAGGCG | | intron 5 5760
 -----+-----+-----+-----+-----+-----+-----+-----+
 N A P R L A N K P K I V F V Q A C R G E
 350 360
 5761 GTTCGTTTTTATTTTAATTTTAATATAAATATTTTAAATAAATTCATTTTCAGAACGTC 5820
 -----+-----+-----+-----+-----+-----+-----+-----+
 R R
 5821 GTGACAATGGATTCCCAGTCTTGGATTCTGTGACGGAGTTCCTGCATTTCTTCGTCGTG 5880
 -----+-----+-----+-----+-----+-----+-----+-----+
 D N G F P V L D S V D G V P A F L R R G
 370 380
 T(n1165)
 5881 GATGGGACAATCGAGACGGGCCATTGTTCAATTTTCTTGGATGTGTGCGGCCGCAAGTTC 5940
 -----+-----+-----+-----+-----+-----+-----+-----+
 W D N R D G P L F N F L G C V R P Q V Q
 390 400
 | intron 6
 5941 AGGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAATCTAAAATAGATTTTT 6000
 -----+-----+-----+-----+-----+-----+-----+-----+
 6001 ATTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC 6060
 -----+-----+-----+-----+-----+-----+-----+-----+
 Repeat 4
 6061 AAACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA 6120
 -----+-----+-----+-----+-----+-----+-----+-----+
 ----->
 6121 GTGAATTGCTGATTGGTCGAGTTTTTCAGTTTAGAGGGAATTTAAAAATCGCCTTTTCGA 6180
 -----+-----+-----+-----+-----+-----+-----+-----+
 6181 AAATTAATAAATTGATTTTTTCAATTTTTTCGAAAAATATTCGATTATTTTATATTCTTT 6240
 -----+-----+-----+-----+-----+-----+-----+-----+

FIGURE 4

A(n717)

6241 GGAGCGAAAGCCCCGTCTTGTAACATTTTTTAAATGATAATTAAATAAATTTTTCAGCAA
-----+-----+-----+-----+-----+-----+-----+
Q

T(n1949)
|

6301 GTGTGGAGAAAAGAAGCCGAGCCAAGCTGACATTCTGATTGCGATACGCAACGACAGCTCAA
-----+-----+-----+-----+-----+-----+-----+
V W R K K P S Q A D I L I R Y A T T A Q
 410 420

A(n1286)
|

6361 TATGTTTCGTGGAGAAAACAGTGTCTCGTGGATCATGGTTCATTCAAGCCGTCTGTGAAGTG
-----+-----+-----+-----+-----+-----+-----+
Y V S W R N S A R G S W F I Q A V C E V
 430 440

T(n1129,n1164)
|

6421 TTCTCGACACACGCAAAGGATATGGATGTTGTTGAGCTGCTGACTGAAGTCAATAAGAAG
-----+-----+-----+-----+-----+-----+-----+
F S T H A K D M D V V E L L T E V N K K
 450 460

T(n2430) A(n2426)
| | | intron 7

6481 GTCGCTTGTTGGATTTCAGACATCACAGGGATCGAATATTTTGAAACAGATGCCAGAGGTA
-----+-----+-----+-----+-----+-----+-----+
V A C G F Q T S Q G S N I L K Q M P E
 470 480

Repeat 5

6541 CTTGAAACAACAATGCATGTCTAACTTTTAAGGACACAGAAAAATAGGCAGAGGCTCCT
-----+-----+-----+-----+-----+-----+-----+

----->

6601 TTTGCAAGCCTGCCGCGCGTCAACCTAGAATTTTAGTTTTTAGCTAAATGATTGATTTT
-----+-----+-----+-----+-----+-----+-----+
6661 GAATATTTTATGCTAATTTTTTTCGGTTAAATTTTGAAATAGTCACTATTTATCGGGTTT
-----+-----+-----+-----+-----+-----+-----+
6721 CCAGTAAAAAATGTTTATTAGCCATTGGATTTTACTGAAAACGAAAAATTGTTAGTTTTTC
-----+-----+-----+-----+-----+-----+-----+
6781 AACGAAATTTATCGATTTTTTAAATGTAAAAAATAAGCGAAAAATTACATCAACCATCAA
-----+-----+-----+-----+-----+-----+-----+
6841 GCATTTAAGCCAAAATTGTTAACTCATTTAAAAATTAATTCAAAGTTGTCCACGAGTATT
-----+-----+-----+-----+-----+-----+-----+
6900

Repeat 5

<-----

6901 ACACGGTTGGCGCGCGCAAGTTTGCAAAACGACGCTCCGCCTCTTTTTCTGTGCGGCTT
-----+-----+-----+-----+-----+-----+-----+
6960

T(n1163)

7020 GAAAAACAAGGGATCGGTTTAGATTTTTCCCCAAAATTTAAATTAAATTTTCAGATGACATC
-----+-----+-----+-----+-----+-----+-----+
M T S

FIGURE 4

7021 CCGCCTGCTCAAAAAGTTCTACTTTTGGCCGGAAGCACGAAACTCTGCCGTCTAAAATTC
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 R L L K K F Y F W P E A R N S A V *
 490 500

7081 ACTCGTGATTCAATTGCCCAATTGATAATTGTCTGTATCTTCTCCCCAGTTCTCTTTCGC
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7080
 7141 CCAATTAGTTTAAAACCATGTGTATATTGTTATCCTATACTCATTTCACCTTTATCATTCT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7140
 7201 ATCATTCTCTTCCCATTTTCACACATTTCATTCTCTACGATAATCTAAAATTATGAC
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7200
 7261 GTTTGTGTCTCGAACGCATAATAATTTAATAACTCGTTTTGAATTTGATTAGTTGTTGT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7260
 7321 GCCCAGTATATATGTATGTACTATGCTTCTATCAACAAAATAGTTTCATAGATCATCACC
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7320
 7381 CCAACCCACCAACCTACCGTACCATATTTCATTTTGC CGGAATCAATTTGATTAATT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7380
 7441 TTAACCTATTTTTCGCCACAAAAATCTAATATTTGAATTAACGAATAGCATTCCCATC
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7440
 7501 TCTCCCGTGCCGGAATGCCTCCCGGCCTTTTAAAGTTTCGGAACATTTGGCAATTATGTAT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7500
 7561 AAATTTGTAGGTCCCCCCCATTTC CGGCCATCATCTCAAATTGCATTCTTTTTCG
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7560
 7621 CCGTGATATCCCGATTCTGGTCAGCAAAGATCT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 7620
 7653

FIGURE 4

004250 26972550

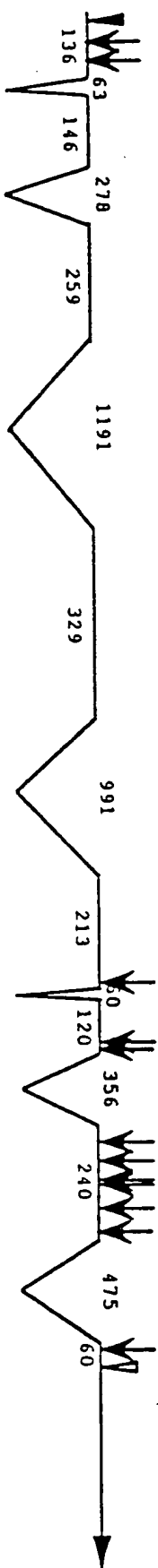


FIGURE 5A

100 90 80 70 60 50 40 30 20 10 0

ced-3 Mutations are Clustered

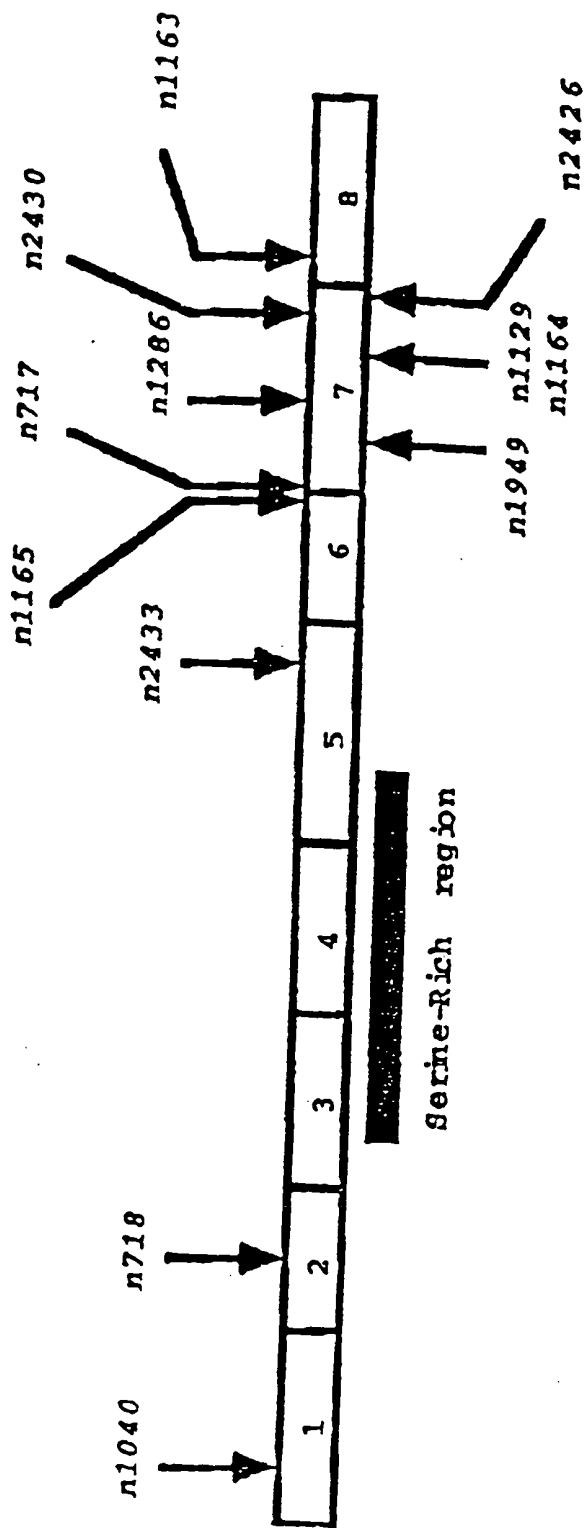


FIGURE 5B

004250 2502450

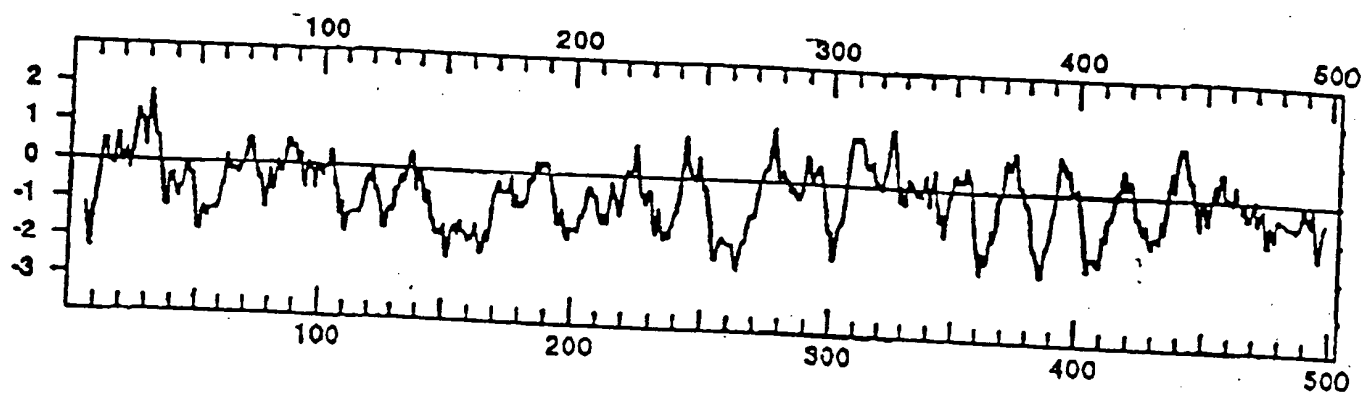


FIGURE 6

Lines

1 01 MMRQDRRSLLERNIMMFSSHLKVDEILEVLIQVLSNDNGDMINSCGTV 50
 2W.....LE...K.QA.L..D.....V....R.E
 3 TVSISLI..R.....M.....

1 51 REKRREIVKAVQRPQGDVAFDAFYDALRSTGHEGLAEVLEPLARSDSNV 100
 2 .DNEK.....R..E.....D...ND..D..M..S.P .P.
 3

1 101 EFECPMSPASHRRSRALSPAGYTSPTVRHRSVSSVSFTS_YQDIYSRA 149
 2 PM.....S.....P .A.....I.....T...V....
 3 S

1 150 RSRSR_SRALHSSDRHNYSSPPVNAFPPSQSSANSSTGCSLGYSSSRN 198
 2 ..S..S..P.Q.....M.AA_TS.....A.....
 3 T..._...P..T.....V..S..S.Q...A.....S.....T

1 199 RSFSKASGPTQYIFHEEDMNEVDAPTISRVEDEKTMYNFSSPRGMCLI 247
 2T.AQS.....Y.....H.....L...
 3 ..Y....AHS.....Y.....H.....T...L...

1 248 INNEHFEQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRD 297
 2I.....E..S...S
 3P...IS.....I.H.....M.....

1 298 FAKHESHGDSAILVILSHGEENVIIGVDDIPSTHEIYDLLNAANAPRLA 347
 2 .GRNDM.....VSVNV.....
 3 ...N.T.....VSVNV...X.....

1 348 NKPKIVFVQACRGERRDNGFPVLDSDGVPAFLRRGWDNRDGPLENFLGC 397
 2L.....SLI.....
 3L.....V.....LI.....KG....

1 398 VRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST 447
 2M..A.....L
 3A.....A.....L

1 448 HAKDMDVVELLTEVNKKVACGFQTSQGSNILKQMPMTSRLKKFYFWPE 497
 2L.....
 3A.....L.....

1 498 _ARN_ SAV 503
 2 DRG.....
 3 _D..RS...

Line 1 C. elegans
 Line 2 C. briggsae
 Line 3 C. vulgaris

FIGURE 7

004260 4634560

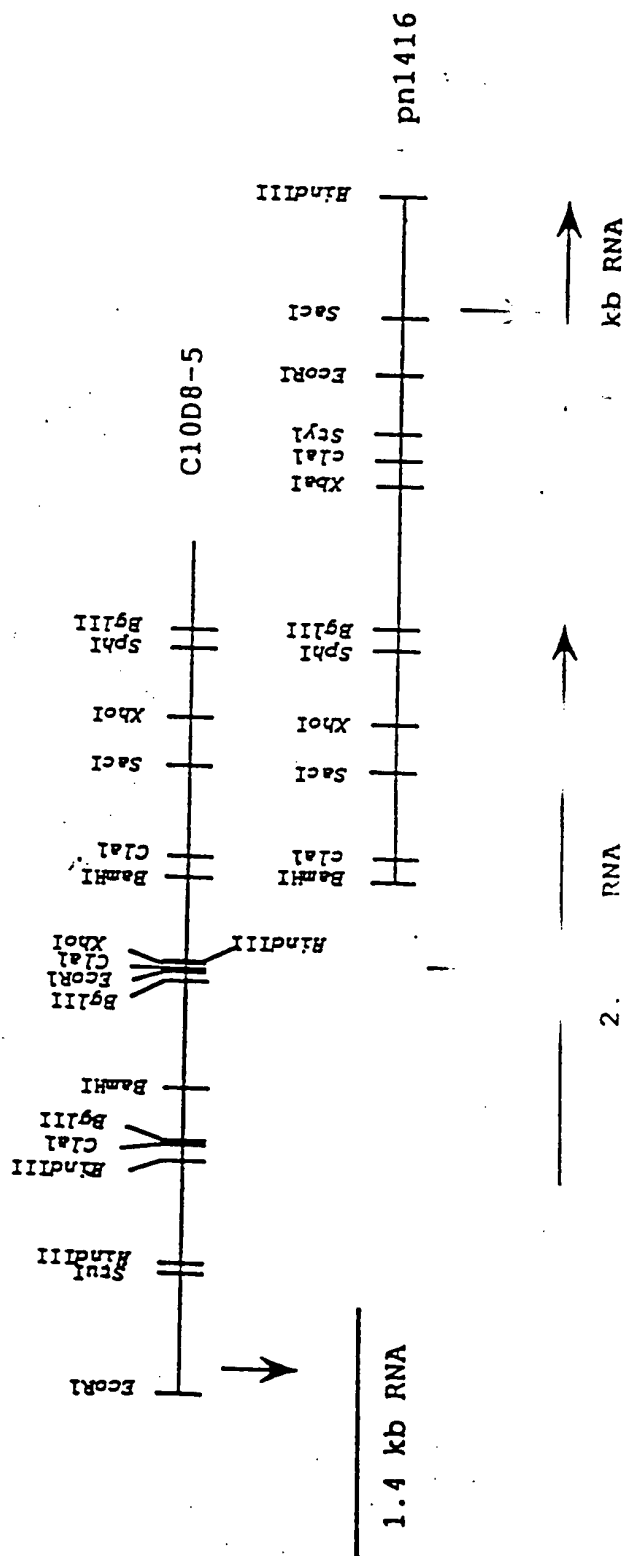


FIGURE 8

IV

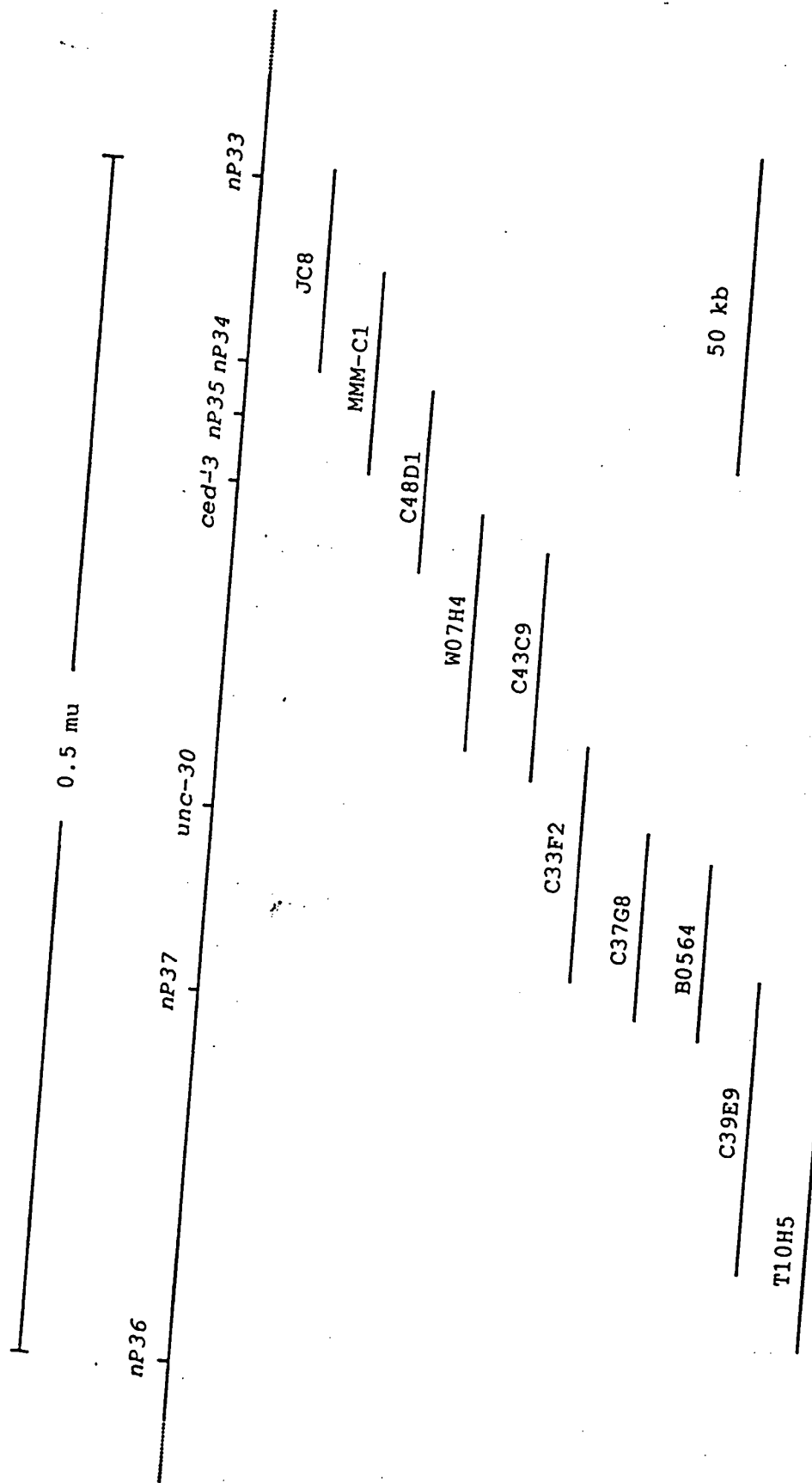


FIGURE 9

Figure 10 Summary of the experiments to localize *ced-3* gene within C40D1.

